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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866)  
217-9197 (toll free).

Reviewer: Keisha Douglas

Timestamp: [year=2009; month=1; day=8; hr=10; min=22; sec=40; ms=875; ]

=====

\*\*\*\*\*

Reviewer Comments:

Glu Leu Leu Asn Ser Met Asn. Ile Ser Gln Pro Thr Val Val Phe Val  
115 120 125

Phe Glu Ala Lys Val Val Asp Leu Asp Thr Gly Lys Thr Leu Gly Val  
370 375 380

Please delete invalid alpha numeric character appearing beside amino acid coding Asn at position 119 in the above sequence id# 39. Please also correct invalid amino acid numbering appearing above at position 375 in the sequence, please check the remaining sequences for similar errors.

Phe Lue Arg Ser Lue Gln Asp Tyr Lys Ile Gln Ser Ala Leu Leu Val  
275 280 285

Please also correct invalid amino acid coding Lue appearing at position 274 and 277 in the above sample of sequence id# 41.

Glu Ala Met Lys Arg Tyr Gly Leu Asn Thr Asn His Arg Ile Val Val  
65 70 75 80

Pro Ile Phe Gly ASn Gln Ile Xaa Pro Asp Thr Ala Ile Leu Ser Val  
225 230 235 240

Per the above sample of sequence id# 42, please correct invalid amino acid numbering at position 75 in the sequence. Please also correct invalid amino acid coding ASn at position 229 in the sequence.

\*\*\*\*\*

Application No: 09763824

Version No: 5.0

Input Set:

Output Set:

Started: 2008-12-24 10:25:15.658

Finished: 2008-12-24 10:25:19.413

Elapsed: 0 hr(s) 0 min(s) 3 sec(s) 755 ms

Total Warnings: 36

Total Errors: 8

No. of SeqIDs Defined: 42

Actual SeqID Count: 42

| Error code | Error Description                                   |
|------------|---|
| W 213      | Artificial or Unknown found in <213> in SEQ ID (1)  |
| W 213      | Artificial or Unknown found in <213> in SEQ ID (2)  |
| W 213      | Artificial or Unknown found in <213> in SEQ ID (3)  |
| W 213      | Artificial or Unknown found in <213> in SEQ ID (4)  |
| W 213      | Artificial or Unknown found in <213> in SEQ ID (5)  |
| W 213      | Artificial or Unknown found in <213> in SEQ ID (6)  |
| W 213      | Artificial or Unknown found in <213> in SEQ ID (7)  |
| W 213      | Artificial or Unknown found in <213> in SEQ ID (8)  |
| W 213      | Artificial or Unknown found in <213> in SEQ ID (9)  |
| W 213      | Artificial or Unknown found in <213> in SEQ ID (10) |
| W 213      | Artificial or Unknown found in <213> in SEQ ID (11) |
| W 213      | Artificial or Unknown found in <213> in SEQ ID (12) |
| W 213      | Artificial or Unknown found in <213> in SEQ ID (13) |
| W 213      | Artificial or Unknown found in <213> in SEQ ID (14) |
| W 213      | Artificial or Unknown found in <213> in SEQ ID (15) |
| W 213      | Artificial or Unknown found in <213> in SEQ ID (16) |
| W 213      | Artificial or Unknown found in <213> in SEQ ID (17) |
| W 213      | Artificial or Unknown found in <213> in SEQ ID (18) |
| W 213      | Artificial or Unknown found in <213> in SEQ ID (19) |
| W 213      | Artificial or Unknown found in <213> in SEQ ID (20) |

**Input Set:**

**Output Set:**

**Started:** 2008-12-24 10:25:15.658  
**Finished:** 2008-12-24 10:25:19.413  
**Elapsed:** 0 hr(s) 0 min(s) 3 sec(s) 755 ms  
**Total Warnings:** 36  
**Total Errors:** 8  
**No. of SeqIDs Defined:** 42  
**Actual SeqID Count:** 42

| Error code | Error Description   |
|------------|---|
|            | This error has occurred more than 20 times, will not be displayed |
| E 330      | Invalid protein , found in SEQID(39) POS (119)Invalid             |
| E 323      | Invalid/missing amino acid numbering SEQID (39)at Protein (375)   |
| E 323      | Invalid/missing amino acid numbering SEQID (39) POS (376)         |
| E 330      | Invalid protein , found in SEQID(41) POS (274)Invalid Protein:Lue |
| E 330      | Invalid protein , found in SEQID(41) POS (277)Invalid Protein:Lue |
| E 323      | Invalid/missing amino acid numbering SEQID (42) POS (73)          |
| E 323      | Invalid/missing amino acid numbering SEQID (42)at Protein (75)    |
| E 330      | Invalid protein , found in SEQID(42) POS (229)Invalid Protein:ASn |

<110> SQUIRRELL, DAVID J.  
MURPHY, MELANIE J.  
PRICE, RACHEL L.  
LOWE, CHRISTOPHER R.  
WHITE, PETER J.  
TISI, LAURENCE C.  
MURRAY, JAMES A. H .

<120> NOVEL ENZYME

<130> 1498-119

<140> 09763824

<141> 2001-02-27

<150> PCT/GB99/03538

<151> 1999-10-26

<150> GB 9823468.5

<151> 1998-10-28

<160> 42

<170> PatentIn Ver. 2.1

<210> 1

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 1

cgccggtgag ctcccgcgcg ccg

23

<210> 2

<211> 23

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer

<400> 2

cgccggcgccg gagctcaccg gcg

23

<210> 3

<211> 51

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 3  
 cgaacacattc ttcatcggtg accgccttaa gtctttaatt aaatacaaag g 51

<210> 4  
 <211> 51  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 4  
 cctttgtatt taattaaaga ctttaaggcgg tcaactatga agaagtgttc g 51

<210> 5  
 <211> 32  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 5  
 gaaagggcccg gcaccagcct atcctctaga gg 32

<210> 6  
 <211> 32  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 6  
 cctctagcgg ataggctggt gccgggcctt tc 32

<210> 7  
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 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 7  
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<210> 8  
 <211> 18  
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<220>  
 <223> Description of Artificial Sequence: Primer

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 gagatacggc gcggttctg g 21  
  
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 <220>  
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 ccaggaaacg cggcgtatct c 21  
  
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 <220>  
 <223> Description of Artificial Sequence: Primer  
  
 <400> 11  
 cccrattttt attctgtggc aaaagcactc 30  
  
 <210> 12  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Primer  
  
 <400> 12  
 gagtgtttt ggcaggaaat gaaaataggg 30  
  
 <210> 13  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Primer  
  
 <400> 13  
 ccgcataagag ctctctgagt caagattc 27

<210> 14  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Primer  
  
 <400> 14  
 gaactctgacg cagagagctc tatgcgg 27  
  
 <210> 15  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Primer  
  
 <400> 15  
 gttgacgcgt tgggatcctt aattaaatac 30  
  
 <210> 16  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Primer  
  
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 gtatagattt gaaaaagac tg 22  
  
 <210> 17  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Primer  
  
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 cagctctttt tcaaatctat ac 22  
  
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 <400> 18  
 ggctacatac tggagacata gc 22  
  
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<211> 22  
 <212> DNA  
 <213> Artificial Sequence  
  
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 <223> Description of Artificial Sequence: Primer  
  
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 gcagttgcgc ccgtgaacga c 21  
  
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 gtgcgtcaag ggagcaactg c 21  
  
 <210> 22  
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 caaatcattc cgggtactgc gattttaag 29  
  
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 <211> 29  
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 <223> Description of Artificial Sequence: Primer  
  
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 cttaaaatcg cagtaccggg aatgatttg 29  
  
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<211> 27  
 <212> DNA  
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 <220>  
 <223> Description of Artificial Sequence: Primer  
  
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 cgcgatagaa ctctctgcgt cagattc 27  
  
 <210> 25  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Primer  
  
 <400> 25  
 gaactctgacg cagagagttc tatgcgc 27  
  
 <210> 26  
 <211> 22  
 <212> DNA  
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 <220>  
 <223> Description of Artificial Sequence: Primer  
  
 <400> 26  
 ctgattacac ccaaggggga tg 22  
  
 <210> 27  
 <211> 22  
 <212> DNA  
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 <220>  
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 <400> 27  
 catcccccctt ggggtgtaac ag 22  
  
 <210> 28  
 <211> 29  
 <212> DNA  
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 <223> Description of Artificial Sequence: Primer  
  
 <220>  
 <221> modified\_base  
 <222> (15)..(17)  
 <223> a, g, c or t  
  
 <400> 28

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cccttcogaa tagannngcc tgcgtcagt                                29

<210> 29
<211> 29
<212> DNA

<213> Artificial Sequence

<220>
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<220>
<221> modified_base
<222> (13)..(15)
<223> a, g, c or t

<400> 29
actgacgcag gccnntctat gcggaaggg                                29

<210> 30
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<220>
<223> Description of Artificial Sequence: Primer

<400> 30
gcaatcaaat cgctccgcat actgc                                    25

<210> 31
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 31
gcagtatccg gagegatttg attgc                                    25

<210> 32
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 32
ccattccatc aaggttttgg                                         20

<210> 33
<211> 20
<212> DNA
<213> Artificial Sequence

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<220>  
 <223> Description of Artificial Sequence: Primer

<400> 33  
 ccaaaacctt gatggaatgg 20

<210> 34  
 <211> 25  
 <212> DNA  
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 <223> Description of Artificial Sequence: Primer

<400> 34  
 aaacagggaac ccatatggaac gaagc 25

<210> 35  
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<400> 35  
 aattaactcg aggaatttcg tcacgcctga atacag 36

<210> 36  
 <211> 30  
 <212> DNA  
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 <223> Description of Artificial Sequence: Primer

<400> 36  
 cccatatttc attctctggcc aaagacactg 30

<210> 37  
 <211> 550  
 <212> PRT  
 <213> Photinus pyralis

<400> 37  
 Met Glu Asp Ala Lys Asn Ile Lys Lys Gly Pro Ala Pro Phe Tyr Pro  
 1 5 10 15

Leu Glu Asp Gly Thr Ala Gly Glu Gln Leu His Lys Ala Met Lys Arg  
 20 25 30

Tyr Ala Leu Val Pro Gly Thr Ile Ala Phe Thr Asp Ala His Ile Glu  
 35 40 45

Val Asn Ile Thr Tyr Ala Glu Tyr Phe Glu Met Ser Val Arg Leu Ala  
 50 55 60

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Ala | Met | Lys | Arg | Tyr | Gly | Leu | Asn | Thr | Asn | His | Arg | Ile | Val | Val | 65  | 70  | 75  | 80  |
| Cys | Ser | Glu | Asn | Ser | Leu | Gln | Phe | Phe | Met | Pro | Val | Leu | Gly | Ala | Leu | 85  | 90  | 95  |     |
| Phe | Ile | Gly | Val | Ala | Val | Ala | Pro | Ala | Asn | Asp | Ile | Tyr | Asn | Glu | Arg | 100 | 105 | 110 |     |
| Glu | Leu | Leu | Asn | Ser | Met | Asn | Ile | Ser | Gln | Pro | Thr | Val | Val | Phe | Val | 115 | 120 | 125 |     |
| Ser | Lys | Lys | Gly | Leu | Gln | Lys | Ile | Leu | Asn | Val | Gln | Lys | Lys | Leu | Pro | 130 | 135 | 140 |     |
| Ile | Ile | Gln | Lys | Ile | Ile | Ile | Met | Asp | Ser | Lys | Thr | Asp | Tyr | Gln | Gly | 145 | 150 | 155 | 160 |
| Phe | Gln | Ser | Met | Tyr | Thr | Phe | Val | Thr | Ser | His | Leu | Pro | Pro | Gly | Phe | 165 | 170 | 175 |     |
| Asn | Glu | Tyr | Asp | Phe | Val | Pro | Glu | Ser | Phe | Asp | Arg | Asp | Lys | Thr | Ile | 180 | 185 | 190 |     |
| Ala | Leu | Ile | Met | Asn | Ser | Ser | Gly | Ser | Thr | Gly | Leu | Pro | Lys | Gly | Val | 195 | 200 | 205 |     |
| Ala | Leu | Pro | His | Arg | Thr | Ala | Cys | Val | Arg | Phe | Ser | His | Ala | Arg | Asp | 210 | 215 | 220 |     |
| Pro | Ile | Phe | Gly | Asn | Gln | Ile | Ile | Pro | Asp | Thr | Ala | Ile | Leu | Ser | Val | 225 | 230 | 235 | 240 |
| Val | Pro | Phe | His | His | Gly | Phe | Gly | Met | Phe | Thr | Thr | Leu | Gly | Tyr | Leu | 245 | 250 | 255 |     |
| Ile | Cys | Gly | Phe | Arg | Val | Val | Leu | Met | Tyr | Arg | Phe | Glu | Glu | Glu | Leu | 260 | 265 | 270 |     |
| Phe | Leu | Arg | Ser | Leu | Gln | Asp | Tyr | Lys | Ile | Gln | Ser | Ala | Leu | Leu | Val | 275 | 280 | 285 |     |
| Pro | Thr | Leu | Phe | Ser | Phe | Phe | Ala | Lys | Ser | Thr | Leu | Ile | Asp | Lys | Tyr | 290 | 295 | 300 |     |
| Asp | Leu | Ser | Asn | Leu | His | Glu | Ile | Ala | Ser | Gly | Gly | Ala | Pro | Leu | Ser | 305 | 310 | 315 | 320 |
| Lys | Glu | Val | Gly | Glu | Ala | Val | Ala | Lys | Arg | Phe | His | Leu | Pro | Gly | Ile | 325 | 330 | 335 |     |
| Arg | Gln | Gly | Tyr | Gly | Leu | Thr | Glu | Thr | Thr | Ser | Ala | Ile | Leu | Ile | Thr | 340 | 345 | 350 |     |
| Pro | Glu | Gly | Asp | Asp | Lys | Pro | Gly | Ala | Val | Gly | Lys | Val | Val | Pro | Phe | 355 | 360 | 365 |     |

Phe Glu Ala Lys Val Val Asp Leu Asp Thr Gly Lys Thr Leu Gly Val  
 370 375 380

Asn Gln Arg Gly Glu Leu Cys Val Arg Gly Pro Met Ile Met Ser Gly  
 385 390 395 400

Tyr Val Asn Asn Pro Glu Ala Thr Asn Ala Leu Ile Asp Lys Asp Gly  
 405 410 415

Trp Leu His Ser Gly Asp Ile Ala Tyr Trp Asp Glu Asp Glu His Phe  
 420 425 430

Phe Ile Val Asp Arg Leu Lys Ser Leu Ile Lys Tyr Lys Gly Tyr Gln  
 435 440 445

Val Ala Pro Ala Glu Leu Glu Ser Ile Leu Leu Gln His Pro Asn Ile  
 450 455 460

Phe Asp Ala Gly Val Ala Gly Leu Pro Asp Asp Asp Ala Gly Glu Leu  
 465 470 475 480

Pro Ala Ala Val Val Val Leu Glu His Gly Lys Thr Met Thr Glu Lys  
 485 490 495

Glu Ile Val Asp Tyr Val Ala Ser Gln Val Thr Thr Ala Lys Lys Leu  
 500 505 510

Arg Gly Gly Val Val Phe Val Asp Glu Val Pro Lys Gly Leu Thr Gly  
 515 520 525

Lys Leu Asp Ala Arg Lys Ile Arg Glu Ile Leu Ile Lys Ala Lys Lys  
 530 535 540

Gly Gly Lys Ser Lys Leu  
 545 550

<210> 38

<211> 550

<212> PRT

<213> Photinus pyralis

<220>

<221> VARIANT

<222> (214)

<223> xaa=an amino acid other than Thr

<400> 38

Met Glu Asp Ala Lys Asn Ile Lys Lys Gly Pro Ala Pro Phe Tyr Pro  
 1 5 10 15

Leu Glu Asp Gly Thr Ala Gly Glu Gln Leu His Lys Ala Met Lys Arg  
 20 25 30

Tyr Ala Leu Val Pro Gly Thr Ile Ala Phe Thr Asp Ala His Ile Glu  
 35 40 45

Val Asn Ile Thr Tyr Ala Glu Tyr Phe Glu Met Ser Val Arg Leu Ala

50

55

60

Glu Ala Met Lys Arg Tyr Gly Leu Asn Thr Asn His Arg Ile Val Val  
65 70 75 80

Cys Ser Glu Asn Ser Leu Gln Phe Phe Met Pro Val Leu Gly Ala Leu  
85 90 95

Phe Ile Gly Val Ala Val Ala Pro Ala Asn Asp Ile Tyr Asn Glu Arg  
100 105 110

Glu Leu Leu Asn Ser Met Asn Ile Ser Gln Pro Thr Val Val Phe Val  
115 120 125

Ser Lys Lys Gly Leu Gln Lys Ile Leu Asn Val Gln Lys Lys Leu Pro  
130 135 140

Ile Ile Gln Lys Ile Ile Ile Met Asp Ser Lys Thr Asp Tyr Gln Gly  
145 150 155 160

Phe Gln Ser Met Tyr Thr Phe Val Thr Ser His Leu Pro Pro Gly Phe  
165 170 175

Asn Glu Tyr Asp Phe Val Pro Glu Ser Phe Asp Arg Asp Lys Thr Ile  
180 185 190

Ala Leu Ile Met Asn Ser Ser Gly Ser Thr Gly Leu Pro Lys Gly Val  
195 200 205

Ala Leu Pro His Arg Xaa Ala Cys Val Arg Phe Ser His Ala Arg Asp  
210 215 220

Pro Ile Phe Gly Asn Gln Ile Ile Pro Asp Thr Ala Ile Leu Ser Val  
225 230 235 240

Val Pro Phe His His Gly Phe Gly Met Phe Thr Thr Leu Gly Tyr Leu  
245 250 255

Ile Cys Gly Phe Arg Val Val Leu Met Tyr Arg Phe Glu Glu Glu Leu  
260 265 270

Phe Leu Arg Ser Leu Gln Asp Tyr Lys Ile Gln Ser Ala Leu Leu Val  
275 280 285

Pro Thr Leu Phe Ser Phe Phe Ala Lys Ser Thr Leu Ile Asp Lys Tyr  
290 295 300

Asp Leu Ser Asn Leu His Glu Ile Ala Ser Gly Gly Ala Pro Leu Ser  
305 310 315 320

Lys Glu Val Gly Glu Ala Val Ala Lys Arg Phe His Leu Pro Gly Ile  
325 330 335

Arg Gln Gly Tyr Gly Leu Thr Thr Thr Ser Ala Ile Leu Ile Thr  
340 345 350

Pro Glu Gly Asp Asp Lys Pro Gly Ala Val Gly Lys Val Val Pro Phe

355

360

365

Phe Glu Ala Lys Val Val Asp Leu Asp Thr Gly Lys Thr Leu Gly Val  
 370 375 380

Asn Gln Arg Gly Glu Leu Cys Val Arg Gly Pro Met Ile Met Ser Gly  
 385 390 395 400

Tyr Val Asn Asn Pro Glu Ala Thr Asn Ala Leu Ile Asp Lys Asp Gly  
 405 410 415

Trp Leu His Ser Gly Asp Ile Ala Tyr Trp Asp Glu Asp Glu His Phe  
 420 425 430

Phe Ile Val Asp Arg Leu Lys Ser Leu Ile Lys Tyr Lys Gly Tyr Gln  
 435 440 445

Val Ala Pro Ala Glu Leu Glu Ser Ile Leu Leu Gln His Pro Asn Ile  
 450 455 460

Phe Asp Ala Gly Val Ala Gly Leu Pro Asp Asp Asp Ala Gly Glu Leu  
 465 470 475 480

Pro Ala Ala Val Val Val Leu Glu His Gly Lys Thr Met Thr Glu Lys  
 485 490 495

Glu Ile Val Asp Tyr Val Ala Ser Gln Val Thr Thr Ala Lys Lys Leu  
 500 505 510

Arg Gly Gly Val Val Phe Val Asp Glu Val Pro Lys Gly Leu Thr Gly  
 515 520 525

Lys Leu Asp Ala Arg Lys Ile Arg Glu Ile Leu Ile Lys Ala Lys Lys  
 530 535 540

Gly Gly Lys Ser Lys Leu  
 545 550

&lt;210&gt; 39

&lt;211&gt; 550

&lt;212&gt; PRT

&lt;213&gt; Photinus pyralis

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; {214}

&lt;223&gt; Xaa=Cys, Ala or Asn

&lt;400&gt; 39

Met Glu Asp Ala Lys Asn Ile Lys Lys Gly Pro Ala Pro Phe Tyr Pro  
 1 5 10 15

Leu Glu Asp Gly Thr Ala Gly Glu Gln Leu His Lys Ala Met Lys Arg  
 20 25 30

Tyr Ala Leu Val Pro Gly Thr Ile Ala Phe Thr Asp Ala His Ile Glu  
 35 40 45

Val Asn Ile Thr Tyr Ala Glu Tyr Phe Glu Met Ser Val Arg Leu Ala  
50 55 60  
Glu Ala Met Lys Arg Tyr Gly Leu Asn Thr Asn His Arg Ile Val Val  
65 70 75 80  
Cys Ser Glu Asn Ser Leu Gln Phe Phe Met Pro Val Leu Gly Ala Leu  
85 90 95  
Phe Ile Gly Val Ala Val Ala Pro Ala Asn Asp Ile Tyr Asn Glu Arg  
100 105 110  
Glu Leu Leu Asn Ser Met Asn. Ile Ser Gln Pro Thr Val Val Phe Val  
115 120 125  
Ser Lys Lys Gly Leu Gln Lys Ile Leu Asn Val Gln Lys Lys Leu Pro  
130 135 140  
Ile Ile Gln Lys Ile Ile Ile Met Asp Ser Lys Thr Asp Tyr Gln Gly  
1